

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 23:06:45 ; Search time 23.77 Seconds
(without alignments)
1423.712 Million cell updates/sec

Title: US-09-497-822a-19
Perfect score: 4912
Sequence: 1 MEVOLGLGRVYPRPFSKTYR.....SVQVPKILSGKVPYVHTQ 923

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Database : SwissProt39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4880	99.3	919	1	ANDR_HUMAN
2	4794	97.6	911	1	ANDR_PANTR
3	4694	95.6	895	1	ANDR_PAPHA
4	4678	95.2	895	1	ANDR_MACFA
5	4404.5	89.7	884	1	ANDR_EULFC
6	4319	87.9	907	1	ANDR_CANFA
7	4200.5	85.5	902	1	ANDR_RAT
8	4176	85.0	899	1	ANDR_MOUSE
9	3509.5	71.4	709	1	ANDR_RABIT
10	1262.5	25.7	930	1	PRGR_RABIT
11	1256	25.6	933	1	PRGR_RAT
12	1234	25.1	923	1	PRGR_RAT
13	1218	24.8	786	1	PRGR_CHICK
14	1205	24.5	923	1	PRGR_MOUSE
15	1116	22.7	377	1	PRGR_SHEEP
16	1092	22.2	981	1	MCR_RAT
17	1078.5	22.0	984	1	MCR_HUMAN
18	1069	21.8	795	1	GCR_RAT
19	1063.5	21.7	783	1	GCR_MOUSE
20	1053.5	21.4	776	1	GCR_XENLA
21	1053.5	21.4	777	1	GCR_SAGO
22	1046.5	21.3	777	1	GCR_AOTNA
23	1042	21.2	777	1	GCR_HUMAN
24	1042	21.2	778	1	GCR_SATSC
25	1041.5	21.2	777	1	GCR_SATBB
26	1034	21.1	612	1	MCR_XENLA
27	1033.5	21.0	776	1	GCR_TUPGB
28	1023	20.8	758	1	GCR_ONCMY
29	1014	20.6	977	1	MCR_TUPGB
30	1005	20.5	807	1	GCR_PAROL
31	996	20.3	771	1	GCR_CAVPO
32	970.5	19.8	703	1	GCR_PIG
33	509	10.4	180	1	PRGR_MACEU

34	502	10.2	595	1	ESR1_PIG	O29040 sus scrofa
35	498.5	10.1	594	1	ESR1_HORSE	O3tv98 equus cabal
36	491	10.0	586	1	ESR1_XENLA	P81559 xenopus lae
37	485.5	9.9	600	1	ESR1_RAT	P06211 rattus norv
38	481	9.8	595	1	ESR1_HUMAN	P03372 homo sapien
39	474.5	9.7	595	1	ESR1_MESAU	Q9qz15 mesocricetu
40	474	9.6	589	1	ESR1_CHICK	P06212 gallus gall
41	474	9.6	599	1	ESR1_MOUSE	P19785 mus musculu
42	470.5	9.6	569	1	ESR1_BRARE	P57717 brachydanio
43	469.5	9.6	622	1	ESR1_ONCMY	P16058 oncorhynchu
44	465	9.5	587	1	ESR1_POEGU	Q91250 poephila gu
45	461.5	9.4	620	1	ESR1_ORYIA	P50241 oryzias lat

ALIGNMENTS

RESULT 1	
ANDR_HUMAN	
ID ANDR_HUMAN	STANDARD; PRT; 919 AA.
AC P10275;	
DT 01-MAR-1989 (Rel. 10, Created)	
DT 01-APR-1990 (Rel. 14, Last sequence update)	
DT 20-AUG-2001 (Rel. 40, Last annotation update)	
DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).	
GN AR OR NR3C4 OR DHTR.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=89112208; PubMed=3216866;	
RA Lubahn D.B., Joseph D.R., Sar M., Tan J., Higgs H.N., Larson R.E.,	
RA French F.S., Wilson E.M.;	
RT "The human androgen receptor: complementary deoxyribonucleic acid	
RL cloning, sequence analysis and gene expression in prostate.";	
RN [2]	
RP SEQUENCE FROM N.A., AND VARIANT CAIS MET-866.	
RX MEDLINE=90083302; PubMed=2594783;	
RA Lubahn D.B., Brown T.R., Simental J.A., Higgs H.N., Migeon C.J.,	
RA Wilson E.M., French F.S.;	
RT "Sequence of the intron/exon junctions of the coding region of the	
RT human androgen receptor gene and identification of a point mutation	
RL in a family with complete androgen insensitivity";	
RN [3]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=90258935; PubMed=2342476;	
RA Govindan M.V.;	
RT "Specific region in hormone binding domain is essential for hormone	
RL binding and trans-activation by human androgen receptor.";	
RN [4]	
RP SEQUENCE FROM N.A.	
RX TISSUE=Prostate;	
RA Chang C., Kokontis J., Liao S.;	
RT "Structural analysis of complementary DNA and amino acid sequences of	
RL human and rat androgen receptors.";	
RN [5]	
RP SEQUENCE FROM N.A.	
RX TISSUE=Prostate;	
RA Tilley W.D., Marcelli M., Wilson J.D., McPhaul M.J.;	
RT "Characterization and expression of a cDNA encoding the human androgen	
RL receptor.";	
RN [6]	
RP SEQUENCE FROM N.A.	
RX TISSUE=Prostate;	

RX MEDLINE=91155943; PubMed=22933020;
 RA Marcelli M., Tilley W.D., Wilson C.M., Griffin J.E., Wilson J.D.,
 RT McPhaul M.J.;
 RT "Definition of the human androgen receptor gene structure permits the
 RT identification of mutations that cause androgen resistance: premature
 RT termination of the receptor protein at amino acid residue 588 causes
 RT complete androgen resistance";
 RL Mol. Endocrinol. 4:1105-1116(1990). X
 RL [7]
 RP SEQUENCE OF 189-919 FROM N.A.
 RP MEDLINE=88178111; PubMed=3353726;
 RX Chang C., Kokontis J., Liao S.;
 RA "Molecular cloning of human and rat complementary DNA encoding
 RT androgen receptors";
 RT Science 240:324-326(1988). ?
 RL [8]
 RP SEQUENCE OF 468-919 FROM N.A.
 RP MEDLINE=88240407; PubMed=3377788;
 RX Trapman J., Klaassen P., Kuiper G.G.J.M., van der Korp J.A.G.M.,
 RA Faber P.W., van Rooij H.C.J., Geurts van Kessel A., Voorhorst M.M.,
 RA Mulder E., Brinkmann A.O.;
 RT "Cloning, structure and expression of a cDNA encoding the human
 RT androgen receptor";
 RL Biochem. Biophys. Res. Commun. 153:241-246(1988). ?
 RL [9]
 RP POLYMORPHISM OF POLY-GLN REGION.
 RP MEDLINE=92220629; PubMed=1561105;
 RX Sladdens H.F.B.M., Oostra B.A., Brinkmann A.O., Trapman J.;
 RA "Trinucleotide repeat polymorphism in the androgen receptor gene
 RT (AR).";
 RT Nucleic Acids Res. 20:1427-1428(1992). X
 RL [10]
 RP POLYMORPHISM OF POLY-GLY REGION.
 RP TISSUE-Blood;
 RA Lu J., Danielson M.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RL [11]
 RP POLYMORPHISM OF POLY-GLN REGION.
 RP MEDLINE=97250535; PubMed=9096391;
 RX Giovannucci E., Stampfer M.J., Krithivas K., Brown M., Brufsky A.,
 RA Talcott J., Hennekens C.H., Kantoff P.W.;
 RT "The CAG repeat within the androgen receptor gene and its
 RT relationship to prostate cancer";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3320-3323(1997). X
 RL [12]
 RP ERRATUM.
 RA Giovannucci E., Stampfer M.J., Krithivas K., Brown M., Dahl D.,
 RA Brufsky A., Talcott J., Hennekens C.H., Kantoff P.W.;
 RL Proc. Natl. Acad. Sci. U.S.A. 94:8272-8272(1997).
 RL [13]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=93092459; PubMed=1458719;
 RA Pinsky L., Trifiro M.A., Kaufman M., Beitel L.K., Mhatre A.,
 RA Kazemi-Esfarjani P., Sabbaghian N., Lumbroso R., Alvarado C.,
 RA Vasiliou M., Gottlieb B.;
 RT "Androgen resistance due to mutation of the androgen receptor";
 RL Clin. Invest. Med. 15:456-462(1992). X
 RL [14]
 RP REVIEW ON VARIANTS AIS.
 RX MEDLINE=93339360; PubMed=8339746;
 RA Brown T.R., Scherer P.A., Chang Y.-T., Migeon C.J., Ghirri P.,
 RA Muroto K., Zhou Z.;
 RT "Molecular genetics of human androgen insensitivity";
 RL Eur. J. Pediatr. 152 Suppl. 2:S62-S69(1993). X
 RL [15]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=94059770; PubMed=8240973;
 RA Sultan C., Lumbroso S., Poujol N., Belon C., Boudon C.,
 RA Lobaccaro J.-M.;
 RT "Mutations of androgen receptor gene in androgen insensitivity
 RT syndromes";
 RL J. Steroid Biochem. Mol. Biol. 46:519-530(1993). X
 RL [16]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=95023089; PubMed=7937057;
 RA Patterson M.N., Hughes L.A., Gottlieb B., Pinsky L.;
 RT "The androgen receptor gene mutations database";
 RL Nucleic Acids Res. 22:3560-3562(1994). X
 RL [17]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=95352489; PubMed=7626493;
 RA Brinkmann A.O., Jenster G., Ris-Stalpers C., van der Korp J.A.G.M.,
 RA Bruggenwirth H.T., Boehmer A.L.M., Trapman J.;
 RT "Androgen receptor mutations";
 RL J. Steroid Biochem. Mol. Biol. 53:443-448(1995). X
 RL [18]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=97169385; PubMed=9016528;
 RA Gottlieb B., Trifiro M.A., Lumbroso R., Vasiliou D.M., Pinsky L.;
 RT "The androgen receptor gene mutations database";
 RL Nucleic Acids Res. 25:158-162(1997). X
 RL [19]
 RP VARIANT LNCAP ALA-877
 RX MEDLINE=91083633; PubMed=2260966;
 RA Veldscholte J., Ris-Stalpers C., Kuiper G.G.J.M., Jenster G.,
 RA Berrevoets C.A., Claassen E., van Rooij H.C.J., Trapman J.,
 RA Brinkmann A.O., Mulder E.;
 RT "A mutation in the ligand binding domain of the androgen receptor of
 RT human LNCap cells affects steroid binding characteristics and
 RT response to anti-androgens";
 RL Biochem. Biophys. Res. Commun. 173:534-540(1990). X
 RL [20]
 RP VARIANTS CAIS CYS-774; GLN-831 AND MET-866.
 RX MEDLINE=91186983; PubMed=2082179;
 RA Brown T.R., Lubahn D.B., Wilson E.M., French F.S., Migeon C.J.,
 RA Corfen J.L.;
 RT "Functional characterization of naturally occurring mutant androgen
 RT receptors from subjects with complete androgen insensitivity";
 RL Mol. Endocrinol. 4:1759-1772(1990). X
 RL [21]
 RP VARIANT CYS-774.
 RX MEDLINE=91310758; PubMed=1856263;
 RA Marcelli M., Tilley W.D., Zoppi S., Griffin J.E., Wilson J.D.,
 RA McPhaul M.J.;
 RT "Androgen resistance associated with a mutation of the androgen
 RT receptor at amino acid 772 (Arg->Cys) results from a combination of
 RT decreased messenger ribonucleic acid levels and impairment of
 RT receptor function";
 RL J. Clin. Endocrinol. Metab. 73:318-325(1991). X
 RL [22]
 RP VARIANT CAIS PRO-617.
 RX MEDLINE=91154385; PubMed=1999491;
 RA Marcelli M., Zoppi S., Grino P.B., Griffin J.E., Wilson J.D.,
 RA McPhaul M.J.;
 RT "A mutation in the DNA-binding domain of the androgen receptor gene
 RT causes complete testicular feminization in a patient with
 RT receptor-positive androgen resistance";
 RL J. Clin. Invest. 87:1123-1126(1991). X
 RL [23]
 RP VARIANT PAIS CYS-763.
 RX MEDLINE=91185626; PubMed=2010552;
 RA McPhaul M.J., Marcelli M., Tilley W.D., Griffin J.E.,
 RA Isidoro-Gutierrez R.F., Wilson J.D.;
 RT "Molecular basis of androgen resistance in a family with a qualitative
 RT abnormality of the androgen receptor and responsive to high-dose
 RT androgen therapy";
 RL J. Clin. Invest. 87:1413-1417(1991). X
 RL [24]
 RP VARIANTS CAIS ASN-695 AND HIS-695, AND SEQUENCE OF 629-723 FROM N.A.
 RX MEDLINE=92131007; PubMed=1775137;
 RA Ris-Stalpers C., Trifiro M.A., Kuiper G.G.J.M., Jenster G., Romalo G.,
 RA Sai T., van Rooij H.C.J., Kaufman M., Rosenfield R.L., Liao S.,
 RA Schweikert H.-U., Trapman J., Pinsky L., Brinkmann A.O.;
 RT "Substitution of aspartic acid-686 by histidine or asparagine in the
 RT human androgen receptor leads to a functionally inactive protein with
 RT altered hormone-binding characteristics";

[illegible]

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AC 097775;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).
GN AR OR NR3C4
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98404153; PubMed=9732460;
RA Choong C.S., Kempainen J.A., Wilson E.M.;
RT "Evolution of the primate androgen receptor: a structural basis for
   disease.";
RL J. Mol. Evol. 47:334-342(1998).X
CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR3 SUBFAMILY.
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DR EMBL; U94177; AAC73048.1; -.
DR HSSP; P06536; IRGD.
DR InterPro; IPR001103; Androgen_recep.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF02166; Androgen_recep; 1.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR PRINTS; PR00521; ANDROGENR.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; znF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT DOMAIN 1 549 MODULATING (BY SIMILARITY).
FT DNA_BIND 551 616 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 551 571 C4-TYPE.
FT ZN_FING 587 611 C4-TYPE.
FT DOMAIN 682 911 LIGAND-BINDING.
FT DOMAIN 57 78 POLY-GLN.
FT DOMAIN 84 88 POLY-GLN.
FT DOMAIN 192 196 POLY-GLN.
FT DOMAIN 371 380 POLY-PRO.
FT DOMAIN 395 401 POLY-ALA.
FT DOMAIN 448 464 POLY-GLY.
SQ SEQUENCE 911 AA; 98402 MW; 601B9BD4E697DAA4 CRC64;

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QY 241 LKAVSVSMGLGVEALHSLSPGQRLGDCMYAPLLGVPAVRPTPCAPLAECCKSLDSDS 300
 Db 222 LKAVSVSMGLGVEALHSLSPGQRLGDCMYAPLLGVPAVRPTPCAPLAECCKSLDSDS 281
 QY 301 AGKSTEDTAYSPFKGYYTKGLEGESLGCSSAAAGSSGTLELPSTLSLYKSGALDEAAA 360
 Db 282 AGKSTEDTAYSPFKGYYTKGLEGESLGCSSAAAGSSGTLELPSTLSLYKSGALDEAAA 341
 QY 361 YQSRDYNFPLALAGPPPPPPHPPHARIKLENPLDYGSAWAAAAQCRYGDLASLHGAG 420
 Db 342 YQSRDYNFPLALAGPPPPPPHPPHARIKLENPLDYGSAWAAAAQCRYGDLASLHGAG 401
 QY 421 AAGPGSGSPSAAASSSHWHLFTAEQOLYXPCGGGGGGGGGGGGGGGGGGGGGGG 480
 Db 402 AAGPGSGSPSAAASSSHWHLFTAEQOLYXPCGGGGGGGGGGGGGGGGGGGGGGG 462
 QY 481 VAPYGYTRPPQGLAGQESDFTAPDVWYPGMVSRVPYPSPTCVKSEMGPMWDSYSGPYGD 540
 Db 453 VAPYGYTRPPQGLAGQESDFTAPDVWYPGMVSRVPYPSPTCVKSEMGPMWDSYSGPYGD 512
 QY 541 MRLETARDHVLPIDYFFPPQKTCCLICGDEASGCHYGALTCGSKVFFKRAAEGKQYLCA 600
 Db 513 MRLETARDHVLPIDYFFPPQKTCCLICGDEASGCHYGALTCGSKVFFKRAAEGKQYLCA 572
 QY 601 SRNDCTIDKFRKNCPSCLRCYKCYEAGMTLGARKLKLGNLKLQEGEASSTTSPTET 660
 Db 573 SRNDCTIDKFRKNCPSCLRCYKCYEAGMTLGARKLKLGNLKLQEGEASSTTSPTET 632
 QY 661 OKLTVSHIGYECQPIFLNVLEAIEPGVVCAGHDNNPDFAALLSSLNELGEROLVHV 720
 Db 633 OKLTVSHIGYECQPIFLNVLEAIEPGVVCAGHDNNPDFAALLSSLNELGEROLVHV 692
 QY 721 KWAKALPGFRNLHVDOMAVIOYQSWGLMVFMAGWRSTNNVSMRYFAPDLVFNERYMH 780
 Db 693 KWAKALPGFRNLHVDOMAVIOYQSWGLMVFMAGWRSTNNVSMRYFAPDLVFNERYMH 752
 QY 781 KSRMYSQCVRMRLHLSQEFGLWQITPOEFLCMKALLFSIIPVDGLKNOKFFDELRMNYIK 840
 Db 753 KSRMYSQCVRMRLHLSQEFGLWQITPOEFLCMKALLFSIIPVDGLKNOKFFDELRMNYIK 812
 QY 841 ELDRIIAKRNKPTSCSRFRFVOLTLLKLDVQPIARELHQFTFDLLIKSHMVSVDFFEMMA 900
 Db 813 ELDRIIAKRNKPTSCSRFRFVOLTLLKLDVQPIARELHQFTFDLLIKSHMVSVDFFEMMA 872
 QY 901 ELISVQVKILSGKVKPIYFHTQ 923
 Db 873 ELISVQVKILSGKVKPIYFHTQ 895

RESULT 4
 ID ANDR_MACFA
 AC 097952; STANDARD; PRT: 895 AA.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).
 GN AR OR NR304.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96404153; PubMed=9732460;
 RA Choong C.S., Kempainen J.A., Wilson E.M.;
 RT "Evolution of the primate androgen receptor: a structural basis for
 disease".
 RL J. Mol. Evol. 47:334-342 (1998).
 CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 CC THE REGULATION OF EUBIOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NR3 SUBFAMILY.
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 CC
 CC EMBL; U94179; AAC73050.1; -;
 DR HSP: P06536; IRGD
 DR InterPro; IPR001103; Androgen_recep.
 DR InterPro; IPR000536; Hormone_rec_lig.
 DR InterPro; IPR001628; zf-C4.
 DR Pfam; PF02166; Androgen_recep; 1.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00047; STROLDIFINGER.
 DR PRINTS; PR00521; ANDROGENR.
 DR SMART; SM00430; HOLI; 1.
 DR SMART; SM00399; ZnF_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 DR Zinc-finger; Steroid-binding.
 KW DOMAIN 1 533 MODULATING (BY SIMILARITY).
 FT ZN_BIND 535 600 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 535 555 C4-TYPE.
 FT ZN_FING 571 595 C4-TYPE.
 FT DOMAIN 666 895 LIGAND-BINDING.
 FT DOMAIN 55 62 POLY-GLN.
 FT DOMAIN 68 74 POLY-GLN.
 FT DOMAIN 178 182 POLY-GLN.
 FT DOMAIN 357 366 POLY-GLN.
 FT DOMAIN 381 387 POLY-ALA.
 FT DOMAIN 434 448 POLY-GLY.
 SQ SEQUENCE 895 AA; 96494 MW; A3EB17916F43A097 CRC64;
 Query Match 95.2%; Score 4678; DB 1; Length 895;
 Best Local Similarity 95.9%; Pred. No. 2.6e-214;
 Matches 886; Conservative 2; Mismatches 6; Indels 30; Gaps 3;
 QY 1 MEVOLGLGRVYPRPPSKTYRGAFQNLFSQSVREVIQNPGRHPPEAASAPPGASLLILQQQ 60
 Db 1 MEVOLGLGRVYPRPPSKTYRGAFQNLFSQSVREVIQNPGRHPPEAASAPPGASL----- 54
 QY 61 QQQ 119
 Db 55 -----QQ 100
 QY 120 QPSALECHPERGCVPEPGAANAASKGLPQQLPAPDEDDSAAPSTLSLGLTFFGLSSC 179
 Db 101 QPSALECHPERGCVPEPGAANAASKGLPQQLPAPDEDDSAAPSTLSLGLTFFGLSSC 160
 QY 180 SADLKILSEASTMQLQQQQQEAIVSESSSGSRRAREASGAPTSSKDNLYLGGTSTISDNK 239
 Db 161 STDLDKILSEASTMQLQQQQQEAIVSESSSGSRRAREASGAPTSSKDNLYLGGTSTISDNK 220
 QY 240 ELCKAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPAVRPTPCAPLAECCKSLDSD 299
 Db 221 ELCKAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPAVRPTPCAPLAECCKSLDSD 280
 QY 300 SAGKSTEDTAYSPFKGYYTKGLEGESLGCSSAAAGSSGTLELPSTLSLYKSGALDEAAA 359
 Db 281 SAGKSTEDTAYSPFKGYYTKGLEGESLGCSSAAAGSSGTLELPSTLSLYKSGALDEAAA 340
 QY 360 YQSRDYNFPLALAGPPPPPPHPPHARIKLENPLDYGSAWAAAAQCRYGDLASLHGAG 419

db 341 AYQSRDYNEFLALAGPPPPPPPPHPPHARIKLENPLDYCSAWAAAAAQCRCYCDLASLHGA 400

QY	420	GAAGSGS	PSAAASSSWHLTFTAEQGLYPCGGGCGGGGGGGGGGGGGGGGAG	479			
Db	401	GAAGFSG	SPSAASSSWHLTFTAEQQLYGFC-----GGGGGGGGGGGAGEAG	451			
QY	480	AVAPYGYTRP	POGLAGOEDEFADPWVPGGMVSRVPSPPTCVKSEGPWMDSYSGPYG	539			
Db	452	AVAPYGYTRP	POGLAGQEDEFADPWVPGGMVSRVPSPPTCVKSEGPWMDSYSGPYG	511			
QY	540	DNRLETARDHVLPI	IDYPPQKTCLICDEASSGHVGALTGCSCKVFVKRAEKGOKYL	599			
Db	512	DNRLETARDHVLPI	IDYFPQKTCLICDEASSGHYGALTCGSKVFFKRAEKGOKYL	571			
QY	600	ASRNDCTIDKFR	RKNPCPSRLRKCYEAGMTLGARKLKLGNLKLOEGEPASSTTPTET	659			
Db	572	ASRNDCTIDKFR	RKNPCPSRLRKCYEAGMTLGARKLKLGNLKLOEGEPASSTTPTET	631			
QY	660	TOKLTVSHIEG	ECOPIFLNVLLEATPGVCAGHDNNQDPSFAALLSSLNELGERQLVHV	719			
Db	632	AQKLTVSHIEG	ECQIFLNVLLEATPGVCAGHDNNQDPSFAALLSSLNELGERQLVHV	691			
QY	720	VKWAKALPGFRNL	HVDQMAVIQYSWMGLMVFMGWRSFTNNSRMXYFAPDLVNEYRM	779			
Db	692	VKWAKALPGFRNL	HVDQMAVIQYSWMGLMVFMGWRSFTNNSRMXYFAPDLVNEYRM	751			
QY	780	HKSRMYSQCVMRHL	SQEGWLQITPQEFCLKALKLLFSIIPVDGLKNOKFFDELRMNYI	839			
Db	752	HKSRMYSQCVMRHL	SQEGWLQITPQEFCLKALKLLFSIIPVDGLKNOKFFDELRMNYI	811			
QY	840	KELDRIITACKRN	NPTSCRRFYOLTLLDSVQPIARELHOFTFDLLIKSHMVSVDPEMM	899			
Db	812	KELDRIITACKRN	NPTSCRRFYOLTLLDSVQPIARELHOFTFDLLIKSHMVSVDPEMM	871			
QY	900	AEIISVOVPKIL	SGKVPIYFHTQ 923				
Db	872	AEIISVOVPKIL	SGKVPIYFHTQ 895				
<hr/>							
RESULT 5							
ANDR_EULFC STANDARD; PRT; 884 AA.							
AC	037776;						
DT	30-MAY-2000 (Rel. 39, Created)						
DT	30-MAY-2000 (Rel. 39, Last sequence update)						
DT	30-MAY-2000 (Rel. 39, Last annotation update)						
DE	ANDROGEN RECEPTOR (DIHYDROTOSTERONE RECEPTOR); AR OR NR3C4.						
OS	Eulemur fulvus collaris (Collared brown lemur).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Eulemur.						
OX	NCBI_TaxId=471178;						
RN	[1]						
RX	SEQUENCE FROM N.A.						
CC	MEDLINE=98404153; PubMed=9732460;						
CC	Cheong C.S., Kempainen J.A., Wilson E.M.;						
RT	"Evolution of the primate androgen receptor: a structural basis for disease".						
RT	J. Mol. Evol. 47:334-342 (1998).						
RL	-!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.						
CC	-!- SUBCELLULAR LOCATION: NUCLEAR.						
CC	-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.						
CC	-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.						
CC	NR3 SUBFAMILY.						
<hr/>							
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U94178; AAC73049.1; -.
 DR HSP; P06536; IRGD.
 DR InterPro; IPR001103; Androgen_recep.
 DR InterPro; IPR000536; Hormone_rec_llig.
 DR InterPro; IPR001628; zf-C4.
 DR Pfam; PF02166; Androgen_recep; 1.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00047; STROIDFINGER.
 DR PRINTS; PR00521; ANDROGENP.
 DR SMART; SM00430; Holi; 1.
 DR SMART; SM00399; ZnF_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Steroid-binding.
 FT DOMAIN 1 522 MODULATING (BY SIMILARITY).
 FT DNA_BIND 524 589 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 524 544 C4-TYPE.
 FT DOMAIN 560 584 C4-TYPE.
 FT DOMAIN 655 884 LIGAND-BINDING.
 FT DOMAIN 55 58 POLY-GLN.
 FT DOMAIN 64 70 POLY-GLN.
 FT DOMAIN 116 120 POLY-ALA.
 FT DOMAIN 174 178 POLY-GLN.
 FT DOMAIN 353 362 POLY-PRO.
 FT DOMAIN 379 383 POLY-ALA.
 FT DOMAIN 408 411 POLY-ALA.
 FT DOMAIN 430 435 POLY-GLY.
 FT SEQUENCE 884 AA; 95610 MW; 18F570E352F4D2BD CRC64;

 Query Match 89.7%; Score 4404.5; DB 1; Length 884;
 Best Local Similarity 90.3%; Pred. No. 2.1e-201; Indels 41; Gaps 3;
 Matches 834; Conservative 20; Mismatches 29;

 QY 1 MEVQLGLGRVYPRPSPKTYRGAFQNLFGSVREVIONPGRHPEAASAAPPGASLLLLQOO 60
 DB 1 MEVQLGLGRVYPRPSPKTYRGAFQNLFGSVREVIONPGRHPEAASAAPPGARL----- 54

 QY 61 OOOOOOOOOOOOOOOOOOOOOOETS-PRQOOOOOGEDGSPQAHRGPTGYLVLDDEEQPS 119
 DB 55 -----OQOOOETSPPOOOOOOGEDGSPQAHRGPTGYLVLDDEEQPS 96

 QY 120 QPOSALCHPGRGCVPEPCAAVAASKGIPQQLPAPPDEDDSAAPTSLSLGPTFPGLSSC 179
 DB 97 QOOSALCHPESCVPPECAAAAASKGLOQOPAPSDDEDDSAVPTSLSLGPTFPGLSSC 156

 QY 180 SADLKDLISEASTMQLLOOQOQEAIVSEGSSSGRAREASGAPTSKONYLGSTISDNAK 239
 DB 157 SADLKDLISEAGTMQLLOOQOQEAIVSEGSSSGRAREAGAPTSKSDSYLGSTISDNAK 216

 QY 240 ELCKAVSVSMGLGVLEAHLSPGEOLRGDMCAPILLGVPPAVRPTPCAPLAECKGSLDD 299
 DB 217 ELCKAVSVSMGLGVETLEHLSFGEQLRGDMCAPILLGVPPAVRPTPCAPLAECKGSLDD 276

 QY 300 SAKGSTEDTAEYSPFGYVTKGLEGESICGSGSAAGSGGTLELPSTLSLYKSGALDEAA 359
 DB 277 SADKGTPEAPYTPFKGYSVTQGLEGESICGSGSAGSGGTLELPSTLSLYKSGALEEA 336

 QY 360 AYQSRDYNEFLALAGPPPPPPHPHARIKLENPLDYGSAAAAAACRYGDLASLHGA 419
 DB 337 SYQSRDYNEFLALAGPPPPPPHPHARIKLENPLDYGSSWAAAAACRYGDLASLHGG 396

 QY 420 GAAGPGSGSPSAAASSSWHTLFTABEGQLYPCGGGGGGGGGGGGGGGGGGGGGGEAG 479
 DB 397 GATPGSGSPSAAASSSWHTLFTABEGQLYPC-----GGGGGGTSEAG 440

 QY 480 AVAPYGYTRPQGLAGQESDFTAPDVMYPGMWVRVYPTCVKSEMGPMWDSYSGPYG 539
 DB 441 AVTPYGYTRPQGLAGQEGDFTAPDVMYPSGVVRVYPTPSCVKSEMGPMWESYSGPYG 500

QY 540 DMRLETARDHVLPIIDYFPQKTCICGDEASGCHYCALTCGCKYVFFKRAAEGKOKYLC 599
 Db 501 DMRLETARDHVLPIIDYFPQKTCICGDEASGCHYCALTCGCKYVFFKRAAEGKOKYLC 560
 QY 600 ASRNDCTIDFRKRNKPCSRKRCYKCYEAGMTLGARKLKLGKLNKLOEGEGASSTTSPTTEET 659
 Db 561 ASRNDCTIDFRKRNKPCSRKRCYKCYEAGMTLGARKLKLGKLNKLOEGEGASSTTSPTTEET 620
 QY 660 TOKLTVSHIEGYECQIFLNLVLAIEPBGVVCAGHNNQDPSFAALLSSNLGGEROLVHV 719
 Db 621 SOKLTVSHIEGYECQIFLNLVLAIEPBGVVCAGHNNQDPSFAALLSSNLGGEROLVHV 680
 QY 720 VKWAKALPGFRNLHVDQMAVIOYSNWGLMVFAMGWRSTFNNSRMLYFAPDLVFNERYM 779
 Db 681 VKWAKALPGFRNLHVDQMAVIOYSNWGLMVFAMGWRSTFNNSRMLYFAPDLVFNERYM 740
 QY 780 HKSRMYSQVVRHSLSOEFGWLQITPOEFLCMKALLFSIIPVDGLKNOKFFDELRMNYI 839
 Db 741 HKSRMYSQVVRHSLSOEFGWLQITPOEFLCMKALLFSIIPVDGLKNOKFFDELRMNYI 800
 QY 840 KELDRIACKRNKPTSCSRREFYOLTLLDVSQVPIARELHOFTFDLLIKSHMYSVDFPEMM 899
 Db 801 KELDRIACKRNKPTSCSRREFYOLTLLDVSQVPIARELHOFTFDLLIKSHMYSVDFPEMM 860
 QY 900 AEIISVQPKILSGKVKPIYFHTQ 923
 Db 861 AEIISVQPKILSGKVKPIYFHTQ 884

RESULT 6
 ANDR_CANFA
 ID ANDR_CANFA STANDARD; PRT; 907 AA.
 AC Q9TT90;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).
 GN AR OR NR3C4.
 OS Canis familiaris (Dog)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lu B., Smock S.L., Castleberry T.A., Owen T.A.;
 RT "Molecular cloning and functional characterization of the canine
 androgen receptor."
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: ANDROGEN RECEPTOR. THE RECEPTORS ARE INVOLVED IN
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NR3 SUBFAMILY.
 CC
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 CC
 CC EMBL; AF197950; AAF18084.1;
 CC InterPro; IPR001103; Androgen_recep.
 CC InterPro; IPR000536; Hormone_rec_lig.
 CC InterPro; IPR001628; zf-C4.
 CC Pfam; PF02166; Androgen_recep; 1.
 CC Pfam; PF00104; hormone_rec; 1.
 CC Pfam; PF00105; zf-C4; 1.

DR SMART; SM00430; HOLI; 1.
 DR SMART; SM00399; znF_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Steroid-binding.
 FT DOMAIN 1 545 MODULATING (BY SIMILARITY).
 FT DNA_BIND 547 612 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 547 567 C4-TYPE.
 FT ZN_FING 583 607 C4-TYPE.
 FT DOMAIN 678 907 LIGAND-BINDING.
 FT DOMAIN 55 64 POLY-GLN.
 FT DOMAIN 70 76 POLY-GLN.
 FT DOMAIN 131 134 POLY-GLN.
 FT DOMAIN 180 202 POLY-GLN.
 FT DOMAIN 329 332 POLY-SER.
 FT DOMAIN 375 384 POLY-PRO.
 FT DOMAIN 399 405 POLY-ALA.
 SQ SEQUENCE 907 AA; 98726 MW; C8619F78DD2338AF CRC64;

Query Match 87.9%; Score 4319; DB 1; Length 907;
 Best Local Similarity 87.3%; Pred. No. 2.3e-197;
 Matches 822; Conservative 20; Mismatches 46; Indels 54; Gaps 5;

QY 1 MEVOLGLGRVYPRPSKTYRGAFONLFQSVREVTONCPRHPEAASAPPGASLLLLQQQ 60
 Db 1 MEVOLGLGRVYPRPSKTYRGAFONLFQSVREVTONCPRHPEAASAPPGASLLLLQQQ 60
 QY 61 QQQ 119
 Db 55 QQQ 102
 QY 120 QPSALECHPERGCVPEFGAANAASKGLPOLPAPPPEDDDSAAPSTLSLGLTFPGLSSC 179
 Db 103 QRSASRGHPESACVPEPGVTSATGKGLQQQPPAPPENDSAAAPSTLSLGLTFPGLSSC 162
 QY 180 SADLKDILSEASTMQLL-----QOOQQQEAESGSSSSGRAREASGAPT 221
 Db 163 STDLDKILSEAGTMQLLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 222
 QY 222 SKDNYLGGTSTISDNAKELCAVSVSMGLGVLEALEHLSPEQLRGDCMYAPLLGVPPAV 281
 Db 223 SKDSYLGGSSTISDSAKELCAVSVSMGLGVLEALEHLSPEQLRGDCMYAPLLGVPPAV 282
 QY 282 RPTPCAPLAECKSLDDSDSAGKSTEDTAETSPKGGYTKGLESGSCSSAAGSGTL 341
 Db 283 R-PCAPLAECKSLDDSDGPGKTEETAETSPKAGYAKGLDGLDGLSCSSSAGSGTL 340
 QY 342 ELPSTLSLYKSGALDEAAAYQSRDYNFPLALAGPPPPPPPPHARIKLENPLDYGSAAW 401
 Db 341 EMPSTLSLYKSGALDEAAAYQSRDYNFPLSLGPPPPPPHARIKLENPLDYGSAAW 400
 QY 402 AAAAAQRYGDLASLHGAGAGGSGSPSAASSSSWHTLFTAEGLYPCGGGGGGGGG 461
 Db 401 AAAAAQRYGDLASLHGAGAGGSGSPSATTSSWHTLFTAEGLYPCGGGGGGGGG 460
 QY 462 GGG 521
 Db 461 DG-----GSVAPGYTRPQGLAGQDEFTAPDVWYPPGVMWVRVPSPT 505
 QY 522 CVKSEMGPMWDSYSGPYGDMRLTARDHVLPIIDYFPQKTCICGDEASGCHYCALTCG 581
 Db 506 CVKSEMGSMWESYSGPYGDMRLTARDHVLPIIDYFPQKTCICGDEASGCHYCALTCG 565
 QY 582 SKVFFKRAEGKQKYLCAASRNCTIDKFRKNCPSCLRKCVEAGMTLGARKLKLGNL 641
 Db 566 SKVFFKRAEGKQKYLCAASRNCTIDKFRKNCPSCLRKCVEAGMTLGARKLKLGNL 625
 QY 642 KLOEGEGASSTTSPTETTKLTSHIEGYECQIFLNLVLAIEPBGVVCAGHNNQDPSF 701
 Db 626 KLOEGEGASNTSPTETTKLTSHIEGYECQIFLNLVLAIEPBGVVCAGHNNQDPSF 685
 QY 702 AALLSSNLGELGRQLVHVVKWAKALPGFRNLHVDQMAVIOYSNWGLMVFAMGWRSTNV 761


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Db 397 AAAACRYGLDASLHGSVAGPTGSPATASSWHTLTAEGQLYGP----- 445
QY 463 GGGGGGGGGGGGAGAVAPYGYTRPPGAGQESDFTAPDWWYVPGMVSRVPSPFC 522
Db 446 ---GGGGSSPSDAGPAPYGYTRPPGAGQESDFTAPDWWYVPGMVSRVPSPSC 501
QY 523 VKSEMGWMDSYSGPYGDMRLTARDHVLPIDYEPPOKTCCLICGDEASGCHYALTCGS 582
Db 502 VKSEMGWMDSYSGPYGDMRLTARDHVLPIDYEPPOKTCCLICGDEASGCHYALTCGS 561
QY 583 CKVFFKRAAEGKOKYLACARNDCIDKFRKNCPCSLRKCCEAGMTLGARKLKLGNLK 642
Db 562 CKVFFKRAAEGKOKYLACARNDCIDKFRKNCPCSLRKCCEAGMTLGARKLKLGNLK 621
QY 643 LOEGEASSTSTTEETOKLVSHTEGECQPIFNVLNLEAEPGVVCAAGHNNQPDSPA 702
Db 622 LOEGEASSTSTTEETOKLVSHTEGECQPIFNVLNLEAEPGVVCAAGHNNQPDSPA 681
QY 703 ALLSSLNGLEROLVHVWAKALPGFRNLHVDDQAVIOYVWMLVFMAGWRFTNVN 762
Db 682 ALLSSLNGLEROLVHVWAKALPGFRNLHVDDQAVIOYVWMLVFMAGWRFTNVN 741
QY 763 SRMLYFAPDLVFNRYMRHKSMTYSCVVRHLSQEFGLQITPQEFCLMKALLFSIIPV 822
Db 742 SRMLYFAPDLVFNRYMRHKSMTYSCVVRHLSQEFGLQITPQEFCLMKALLFSIIPV 801
QY 823 DGLKNOKFDELNMVYKELDRILIAKRNKPTSCSRFFVQLTKLSDVOPIARELHQFTF 882
Db 802 DGLKNOKFDELNMVYKELDRILIAKRNKPTSCSRFFVQLTKLSDVOPIARELHQFTF 861
QY 883 DLLIKSHMVSDVPEMMAEIIISVQVKILSGVKPIYFHTQ 923
Db 862 DLLIKSHMVSDVPEMMAEIIISVQVKILSGVKPIYFHTQ 902

RESULT 8
ID ANDR_MOUSE STANDARD; PRT; 899 AA.
AC P19091;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANDROGEN RECEPTOR (Q1HYDROTESTOSTERONE RECEPTOR).
GN AR OR NR3C4.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=90386642; PubMed=2403358;
RA He W.W., Fischer L.M., Sun S., Bilhartz D.L., Zhu X., Young C.Y.F.,
RA Kelley D.B., Tindall D.J.;
RT "Molecular cloning of androgen receptors from divergent species with
RT a polymerase chain reaction technique: complete cDNA sequence of the
RT mouse androgen receptor and isolation of androgen receptor cDNA
RT probes from dog, guinea pig and clawed frog."
RL Biochem. Biophys. Res. Commun. 171:697-704(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91133433; PubMed=2178222;
RA Gaspar M.L., Neo T., Tosi M.;
RT "Structure and size distribution of the androgen receptor mRNA in
RT wild-type and Tfm/Y mutant mice."
RL Mol. Endocrinol. 4:1600-1610(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91354214; PubMed=1883336;
RA Faber P.W., King A., van Rooij H.C.J., Brinkmann A.O., de Both N.J.,
RA Trapman J.;
RT "The mouse androgen receptor. Functional analysis of the protein and

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RT RT
RL RT
RN RT
RP RT
RX RT
RA RT
RA French F.S.;
RT "A frameshift mutation destabilizes androgen receptor messenger RNA
RT in the Tfm mouse."
RL Mol. Endocrinol. 5:573-591(1991).
CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -!- MISCELLANEOUS: IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS
CC ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS;
CC HORMONE BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE
CC HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA
CC SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR3 SUBFAMILY.
CC
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CC -----
CC EMBL; S56585; AAB19916.1; -
CC EMBL; X53779; CAA37795.1; -
CC EMBL; M37890; AAA37234.1; -
CC EMBL; X59592; CAA42160.1; -
CC PIR; A35895; A35895;
CC PIR; A37255; A37255;
CC PIR; A37908; A37908;
CC PIR; S17198; S17198;
CC PIR; S34398; S34398;
CC HSSP; P06536; 1RGD.
CC TRANSFAC; T00041; -
CC MGD; MGI:88064; Ar.
CC InterPro; IPR001103; Androgen_recep.
CC InterPro; IPR000536; Hormone_rec_llg.
CC InterPro; IPR001628; zf-C4.
CC Pfam; PF02166; Androgen_recep; 1.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00047; STROIDFINGER.
CC PRINTS; PR00521; ANDROGENR.
CC SMART; SM00430; HOL1; 1.
CC SMART; SM00399; ZnF_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Steroid-binding.
FT DOMAIN 1 537 MODULATING (BY SIMILARITY).
FT DNA_BIND 539 604 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 539 559 C4-TYPE.
FT ZN_FING 575 599 C4-TYPE.
FT DOMAIN 670 899 LIGAND-BINDING.
FT DOMAIN 63 67 POLY-ARG.
FT DOMAIN 174 193 POLY-GLN.
FT DOMAIN 367 373 POLY-PRO.
FT DOMAIN 391 397 POLY-ALA.
FT DOMAIN 441 447 POLY-GLY.
SQ SEQUENCE 899 AA; 98193 MW; FD9E07C07F7A568 CRC64;

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Query Match 85.0%; Score 4176; DB 1; Length 899;
 Best Local Similarity 84.1%; Pred. No. 1.3e-190;
 Matches 790; Conservative 40; Mismatches 53; Indels 56; Gaps 5;

QY 1 MEVQLGLGRVYPRPPSKTYGAFQNLFSQSVREVIQNGPRHPPEASAAAPPASGLLLQQQ 60
 Db 1 MEVQLGLGRVYPRPPSKTYGAFQNLFSQSVREVIQNGPRHPPEASAAAPPASGLLLQQQ 54
 QY 61 QQQ 119
 Db 55 -----QORQTSPPRRRROQHTEDGSPQAHIRGTGYLALEEEQQPS 96
 QY 120 QPQALRECHBERGCVPPGAAVASKGLPOOLPAPDEDDSAAPSTLSLGLTFFPGLSSC 179
 Db 97 QQAASCHPESSCLPPEGAATAPGKLPQPPAPPDQDDSAAPSTLSLGLTFFPGLSSC 156
 QY 180 SADLKDILSEASTMOLLQ-----QQQQAASCHPESSCLPPEGAATAPGKLPQPPAP 224
 Db 157 SADLKDILSEASTMOLLQ-----QQQQAASCHPESSCLPPEGAATAPGKLPQPPAP 215
 QY 225 DNYLGGTSTISDNAKELCKAVSMGLGVLEHLSPEGEOLRDCMYAPLLGVPPAVRPT 284
 Db 216 DSYLGGNSTISDNAKELCKAVSMGLGVLEHLSPEGEOLRDCMYAPLLGVPPAVRPT 275
 QY 285 PCAPLAECKSLDSDSAGKSTEDTAESYPPKGYTYKLGESLGCSSGAAGSGTLELP 344
 Db 276 PCAPLAECKSLDSDSAGKSTEDTAESYPPKGYTYKLGESLGCSSGAAGSGTLELP 335
 QY 345 STLSLYKSGALDEAAAYQSDRYNFPALAGPPPPPPPPHARIKLENPDLGYSAWAAA 404
 Db 336 SSLSLYKSGALDEAAAYQSDRYNFPALAGPPPPPPPPHARIKLENPDLGYSAWAAA 395
 QY 405 AAQCRYGDLASLHGAAGPCGSPSAASSSWHTLFTAEEOGLYPCGGGGGGGGGGG 464
 Db 396 AAQCRYGDLASLHGAAGPCGSPSAASSSWHTLFTAEEOGLYPCGGGGGGGGGGG 442
 QY 465 GGGGGGGGGGGGAGAVAPYGYTRPPQCLAGQSDFTAPDVPVPGMWSRVYPPSPCVK 524
 Db 443 --GGGGSSSPSDAGVAPYGYTRPPQCLAGQSDFTAPDVPVPGMWSRVYPPSPCVK 500
 QY 525 SEMGPWMDSYSGPYGDMRLTARDHVLPIDYFPPOKTCILCDEASGCHYGALTCGSK 584
 Db 501 SEMGPWMDSYSGPYGDMRLTARDHVLPIDYFPPOKTCILCDEASGCHYGALTCGSK 560
 QY 585 VFFKRAEGKQKYLACARNCTIDKFRKNCPCSRURKCYEAGMTLGARKKLKGLNKLQ 644
 Db 561 VFFKRAEGKQKYLACARNCTIDKFRKNCPCSRURKCYEAGMTLGARKKLKGLNKLQ 620
 QY 645 EGEASTTSPTTEKTLVSHTEGVECOPIFLNVLEATEPGVVCAGHNNOPDSFAAL 704
 Db 621 EGENSNAGSPTEPDSPKMTVSHTEGVECOPIFLNVLEATEPGVVCAGHNNOPDSFAAL 680
 QY 705 LSSLNELGERQLVHVVKAKALPFRNLHVDQMAVITYQSWMGLMVFAMGWSRFTNVNSR 764
 Db 681 LSSLNELGERQLVHVVKAKALPFRNLHVDQMAVITYQSWMGLMVFAMGWSRFTNVNSR 740
 QY 765 MLYFAPDLVFNEMRHKSRMYSOCVRMRHLISQEFGLQITPQEFGLMCKALLLSIIPVDG 824
 Db 741 MLYFAPDLVFNEMRHKSRMYSOCVRMRHLISQEFGLQITPQEFGLMCKALLLSIIPVDG 800
 QY 825 LKNQKFFDELRMNVIKELDRILACKRNKPTSCSRFFVQLTKLSDSQVPIARELHQFTFDL 884
 Db 801 LKNQKFFDELRMNVIKELDRILACKRNKPTSCSRFFVQLTKLSDSQVPIARELHQFTFDL 860
 QY 885 LKSHMYSVDFPEMMAEIIISVQVFKILSGVKVPIYFHTQ 923
 Db 861 LKSHMYSVDFPEMMAEIIISVQVFKILSGVKVPIYFHTQ 899

RESULT 9

ID ANDR_RABIT STANDARD; PRT; 709 AA.
 AC P49699;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR) (FRAGMENT).
 GN AR OR NR3C4.
 OS Oryctolagus cuniculus (Rabbit)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN NCBI_TaxID=9986;
 RL 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEW ZEALAND WHITE; TISSUE=Prostate;
 RC MEDLINE=96044663; PubMed=7559153;
 RA Krongrad A., Wilson J.D., McPhaul M.J.;
 RT "Cloning and partial sequence of the rabbit androgen receptor:
 RT expression in fetal urogenital tissues.";
 RL J. Androl. 16:209-214 (1995).
 CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NR3 SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; U16366; AAC48469.1; -.
 DR HSP: P06536; IRGD.
 DR InterPro: IPR001103; Androgen_recep.
 DR InterPro: IPR000536; Hormone_rec_119.
 DR InterPro: IPR001628; zf-C4.
 DR Pfam: PF02166; Androgen_recep; 1.
 DR Pfam: PF00104; hormone_rec; 1.
 DR Pfam: PF00105; zf-C4; 1.
 DR SMART; SM00430; HOLI; 1.
 DR SMART; SM00339; ZnF_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW zinc-finger; Steroid-binding.
 FT NON_TER 1 1
 FT DOMAIN <1 347 MODULATING.
 FT DNA_BIND 349 414 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 349 369 C4-TYPE.
 FT ZN_FING 385 409 C4-TYPE.
 FT DOMAIN 480 709 LIGAND-BINDING.
 FT DOMAIN 3 6 POLY-GLN.
 FT DOMAIN 182 187 POLY-PRO.
 FT DOMAIN 201 207 POLY-ALA.
 FT DOMAIN 254 262 POLY-GLY.
 FT SEQUENCE 709 AA; 77391 MW; 40E7666137E97B6B CRC64;
 SQ
 Query Match 71.4%; Score 3509.5; DB 1; Length 709;
 Best Local Similarity 90.9%; Pred. No. 3.1e-159;
 Matches 660; Conservative 16; Mismatches 31; Indels 19; Gaps 3;
 QY 198 QQQQAVSEGGSSSGRRAREASGAPTSSKDNYLGGTSTISDNAKELCKAVSMGLGVLEA 257
 Db 3 QQQQDAATEGSSSGRRARRPSGASTSSKDSYLGSTSVISDSAKELCKAVSMGLGVLEA 62
 QY 258 HLSPEQLRGDCMYAPILCVPAVRPTCAPLAECKSLDSDSAGKSTEDTAESYPPKGG 317
 Db 63 HUSSGEQLRGDCMYAPILGGPPVVRPTCLPLVECKSLDSDGPKGTETAEYTPKGG 122
 QY 318 YTKGLGEGSLGCGSAAAGSGGTLEPSTLSLYKSGALDEAAAYQSDRYNFPALAGPP 377
 Db 123 YNKGLEASLGCSSGSEAGSSCTLEPSTLSLYKSGTLDAAAYQTRDYNYNFPALAG-- 180


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QY 250 GLGV-----EALHLSPEQLRGDCM-----YAPLLGV 277
Db 285 DAPVAPGRSPLATTVVDFIHPILPLNHALAARTOLLEGSDYDGGAAAVPFAPPRGS 344
QY 278 PPAVR-PTCAPLAECKSLDDSGAKSTED-TABYSFPKGGYTKLGESLGCSSAAA 335
Db 345 PSAPSPVPCGDFPDC-----TYPPEGDPKEDGFPVYGFQPPGLAIKEE-----EGTEAA 396
QY 336 GSSGTELEPSTLSLYKSGALDEAAAYQSRDYNNFLALAGPPPP-PPPHPHARIKLEN 393
Db 397 SRS-----PRPYLL-----AGASAATFPDFPL-----PRPPRAPPSRP----- 430
QY 394 PLDYGSAMAAAAOQRYGLAS-----LHGAGAAFGSGS-----PSAAASSSWH 438
Db 431 ----GEA-AVAAPSAVSPVSSGSALECILYKABGAPPTQGSFAPLCKPPAASS----- 481
QY 439 TLFTAEEGOLYPCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 498
Db 482 -CLLPDRSLPAAP-----TSSAAPAIY--PPLGLNG-- 509
QY 499 DFTAPDVWYPGGMV-SRVPYPSPTCVKSEMGPWMD-----SYSGPYGDMRLTARDH 549
Db 510 ---LQLGQAVALKDSLPOVYP-----PYLNLRPDSEASQSPQYGFDSL----- 552
QY 550 VLPIDYFPPOKTLICGDEASGCHYGALTCGCKVFKAAGKQKYLCAASRNDCTIDK 609
Db 553 -----POKICLICGDEASGCHYGVLTCGCKVFKAAGKQKYLCAASRNDCTIDK 603
QY 610 FRKNCPSRLKCKYACMTLGARKLKLGNLKLQE--EGEA--SSTTSPTTEWT--OKL 663
Db 604 TRKNCPCACRLKCKYACMTLGARKLKLGNLKLQE--EGEA--SSTTSPTTEWT--OKL 663
QY 664 TVSHIEGYECOPIFLNLLEATEPVGVCAGHDNQPDSFAALLSSNLGELQVHVVKWA 723
Db 664 TFSNQETQLVPLINLILMSLEPDDVYAGHNTKPDTSLSLLTSLNOLGERQLSVVVKWS 723
QY 724 KALPGFRLHVDQNAVTOYQSWGLMVFAMGWSFTWNSRMLYFADPLVFNRYMHKSR 783
Db 724 KSLPGFRLHVDQNAVTOYQSWGLMVFAMGWSFTWNSRMLYFADPLVFNRYMHKSR 783
QY 784 MYSQVVRHRLSHQFGLWLOITPQFEELCKMALLFSITPDGLKNQKFFDLRWNKYKELD 843
Db 784 FYSLLKRWQIPQEFVKQVTHEEFLCKMALLLNTLPLEGLRSQSOFEMRSYIRELI 843
QY 844 RIACKRNKPTSCRRRYQLTKLDSVQPIARELHOFTFDLLIKSHMVSVDFPEMMAEII 903
Db 844 KAIGLRQKGVVPSQRFYQLTKLDSLHLVQLHLYCLNTFTIQSALAVFEPEMMAEVI 903
QY 904 SVQVPKILSGVKPIYFH 921
Db 904 AAQUPKILAGMVKPLLFH 921

RESULT 13
PRGR_CHICK
ID PRGR_CHICK STANDARD; PRT; 786 AA.
AC P07812; Q90946;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROGESTERONE RECEPTOR (PR).
GN PCR OR NR3C3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166640; PubMed=3443098;
RA Gronemeyer H., Turcotte B., Quirin-Stricker C., Bocquel M.T.,
RA Meyer M.E., Krozowski Z., Jeltsch J.M., Lerouge T., Garnier J.M.,
RA Chambon P.;
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RT "The chicken progesterone receptor: sequence, expression and
RT functional analysis.";
RL EMBO J. 6:3985-3994(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91042592; PubMed=3153474;
RA Conneely O.M., Dobson A.D.W., Tsai M.-J., Beattie W.G., Toft D.O.,
RA Hucky C.S., Zarucki T., Schrader W.T., O'Malley B.W.;
RT "Sequence and expression of a functional chicken progesterone
RT receptor.";
RL Mol. Endocrinol. 1:517-525(1987).
RN [3]
RP SEQUENCE OF 128-164 FROM N.A.
RX MEDLINE=86289413; PubMed=2426779;
RA Conneely O.M., Sullivan W.P., Toft D.O., Birnbaumer M., Cook R.G.,
RA Maxwell B.L., Zarucki-Schulz T., Greene G.L., Schrader W.T.,
RA O'Malley B.W.;
RT "Molecular cloning of the chicken progesterone receptor.";
RL Science 233:767-770(1986).
RN [4]
RP SEQUENCE OF 417-490 FROM N.A.
RX MEDLINE=86287271; PubMed=2426697;
RA Jeltsch J.M., Krozowski Z., Quirin-Stricker C., Gronemeyer H.,
RA Simpson R.J., Garnier J.M., Krust A., Jacob F., Chambon P.;
RT "Cloning of the chicken progesterone receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5424-5428(1986).
RN [5]
RP DIFFERENCE BETWEEN FORM 1 AND FORM 2.
RX MEDLINE=89340509; PubMed=2760059;
RA Conneely O.M., Kettelberger D.M., Tsai M.-J., Schrader W.T.,
RA O'Malley B.W.;
RT "The chicken progesterone receptor A and B isoforms are products of
RT an alternate translation initiation event.";
RL J. Biol. Chem. 264:14062-14064(1989).
RN [6]
RP SEQUENCE FROM N.A. (ALL FORMS).
RX MEDLINE=90154085; PubMed=2303488;
RA Jeltsch J.-M., Turcotte B., Garnier J.-M., Lerouge T., Krozowski Z.,
RA Gronemeyer H., Chambon P.;
RT "Characterization of multiple mRNAs originating from the chicken
RT progesterone receptor gene. Evidence for a specific transcript
RT encoding form A.";
RL J. Biol. Chem. 265:3967-3974(1990).
CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE), A', B AND B';
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: OVIDUCT.
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR3 SUBFAMILY.
CC -----
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CC -----
DR EMBL; Y00092; CAA68282.1; -
DR EMBL; M13972; AAA49034.1; -
DR EMBL; M37518; AAA49013.1; -
DR EMBL; M37518; AAA49014.1; -
DR EMBL; M14278; AAA49035.1; -
DR EMBL; M14279; AAA49038.1; -
DR EMBL; M14280; AAA49039.1; -
DR EMBL; M32732; AAA49011.1; -
DR EMBL; M31104; AAA49011.1; JOINED.
DR EMBL; M32726; AAA49011.1; JOINED.
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Qy	13	RPSKTYRGAFQNFOSVREVTONGPR-HPEANAASAPPGCASLLLLQOQQOQQOQQOQQO 71
Db	10	RAPSSARDGAV-----LIQAPESRGEAGIDVALDG-----LLYPRSSDEEEEEENE 57
Qy	72	QOQOQOQOQOQOETSPRQOQOQOQOQEDGSPQARRGPTGYLVLDDEQQPSQPSALECHP 131
Db	58	EEEEEEEPQORE-----EEEEEEEDRDCFSYR----- 85
Qy	132	GCVPPEGAAVAASKGULPQQLPAPBEDDSSAAPST---LSLIGPTPPGLSSCSADLKDL 187
Db	86	-----PGGSLSKDCLDSVL-----DTFLAPAAHAAPWSLFGPEVP----- 121
Qy	188	SEASTMOLLQOQOQOEAVSEQ-SSSGRAREASGAPTSSKKNYLGTTISDNAKELCKAYS 246
Db	122	-EVPVAPMSRGPTOKAVDAGPGAPGSPQPRGAP-----LWPGADSLNVAVK 167
Qy	247	VSMGLGVEALEHLSPGBQLRGDCMYAPLLGVVPVAVRPTPCAPLAIECKGSLLLDDSGAKSTE 306
Db	168	ARPG-PEDASENRAPG-----LPGAEERGGPPEPDA----- 196

RESULT	14
PRGR_MOUSE	
ID	PRGR_MOUSE STANDARD; PRRT; 923 AA.
AC	Q00175;
DT	01-DEC-1992 (Rel. 24, Created)
DT	01-DEC-1992 (Rel. 24, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	FROGESTERONE RECEPTOR (PR).
GN	PGR OR NR3C3 OR PR.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=D1299759; PubMed=2069958;
RA	Schott D.R., Shyamala G., Schneider W., Parry G.;
RT	"Molecular cloning, sequence analyses, and expression of
RT	complementary DNA encoding murine progesterone receptor.";
RL	Biochemistry 30:7014-7020(1991).
RN	[2]
RP	SEQUENCE OF 1-9 FROM N.A.
RC	STRAIN=129/SV;
RX	MEDLINE=G95100931; PubMed=7802637;

